

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: November 15, 2007, 08:50:16 ; Search time 193 Seconds
(without alignments)
88.954 Million cell updates/sec

Title: US-10-568-108-1

Perfect score: 76

Sequence: 1 LRRERQSRRLRERQSR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_8.4:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
--------	-------	-----	-------	-------	--------	----	----	-------------

1	52	68.4	2753	2	Q3KN34_DROME			Q3kn34 drosophila
2	52	68.4	2935	2	Q7Z1Y4_DROME			Q7z1y4 drosophila
3	52	68.4	2946	2	Q9W053_DROME			Q9w053 drosophila
4	51	67.1	513	2	Q9DEG2_CHICK			Q9deg2 gallus gall

5	51	67.1	526	2	Q5XHX3_RAT	Q5xhx3 ratus norv
6	51	67.1	550	2	O93263_CHICK	O93263 gallus gall
7	51	67.1	784	2	Q90YB5_CHICK	Q90yb5 gallus gall
8	51	67.1	802	1	ENAH_MOUSE	Q03173 mus musculu
9	50	65.8	320	2	Q4DK01_TRYCR	Q4dk01 trypanosoma
10	50	65.8	391	2	Q4CTG4_TRYCR	Q4ctg4 trypanosoma
11	50	65.8	591	1	ENAH_HUMAN	Q8n8s7 homo sapien
12	49	64.5	359	2	Q16LV4_AEDAE	Q16lv4 aedes aegyp
13	49	64.5	1190	2	Q519A0_ENTHI	Q519a0 entamoeba h
14	49	64.5	1439	2	Q5CQG9_CRYPV	Q5cqg9 cryptospori
15	49	64.5	1898	1	TRHY_HUMAN	Q07283 homo sapien
16	49	64.5	1943	2	Q5VUI3_HUMAN	Q5vui3 homo sapien
17	48	63.2	260	2	Q5ZD80_ORYSA	Q5zd80 oryza sativ
18	48	63.2	372	2	Q6DUB6_PIG	Q6dub6 sus scrofa
19	48	63.2	523	2	Q5RHP5_BRARE	Q5rhp5 brachydanio
20	48	63.2	527	1	GCP60_HUMAN	Q9h3p7 h golgi res
21	48	63.2	540	2	Q2J1R0_RHOP2	Q2j1r0 rhodopseudo
22	48	63.2	668	2	Q57VZ5_9TRYP	Q57vz5 trypanosoma
23	48	63.2	685	1	CS021_PONPY	Q5rbh3 pongo pygma
24	48	63.2	1094	2	Q26774_9TRYP	Q26774 trypanosoma
25	48	63.2	1784	2	Q54TU2_DICDI	Q54tu2 dictyosteli
26	48	63.2	1914	2	Q3GJD8_CHLPH	Q3gjd8 prosthecoch
27	47	61.8	154	2	Q6YTG1_ORYSA	Q6ytg1 oryza sativ
28	47	61.8	359	2	Q5Z6A2_ORYSA	Q5z6a2 oryza sativ
29	47	61.8	524	1	GCP60_MOUSE	Q8bmp6 m golgi res
30	47	61.8	544	2	Q5B8X7_EMENI	Q5b8x7 emericella
31	47	61.8	545	2	Q4CVF8_TRYCR	Q4cvf8 trypanosoma
32	47	61.8	545	2	Q4CMJ9_TRYCR	Q4cmj9 trypanosoma
33	47	61.8	791	2	Q26LI9_XANP2	Q26li9 xanthobacte
34	47	61.8	800	2	Q9Y102_DROME	Q9y102 drosophila
35	47	61.8	925	2	Q2QNZ9_ORYSA	Q2qnz9 oryza sativ
36	47	61.8	971	2	Q6C1S3_YARLI	Q6c1s3 yarrowia li
37	47	61.8	1046	2	Q3JNP6_BURP1	Q3jnp6 burkholderi
38	47	61.8	1229	2	Q6C1W6_YARLI	Q6c1w6 yarrowia li
39	47	61.8	2486	2	Q9VXM5_DROME	Q9vxm5 drosophila
40	46	60.5	117	2	Q9VNS4_DROME	Q9vns4 drosophila
41	46	60.5	129	2	Q9VNS6_DROME	Q9vns6 drosophila
42	46	60.5	289	1	CWC23_SCHPO	Q9p7c6 schizosacch
43	46	60.5	298	2	Q1LZ42_DROME	Q1lz42 drosophila
44	46	60.5	399	2	Q510K9_ENTHI	Q510k9 entamoeba h
45	46	60.5	436	2	Q624C9_CAEBR	Q624c9 caenorhabdi
46	46	60.5	536	2	Q50N21_ENTHI	Q50n21 entamoeba h
47	46	60.5	537	2	Q9U3Z8_ENTHI	Q9u3z8 entamoeba h
48	46	60.5	564	2	Q4SFM4_TETNG	Q4sfm4 tetraodon n
49	46	60.5	586	2	Q34WM2_9GAMM	Q34wm2 alkalilimni
50	46	60.5	589	2	Q1EA13_CO CIM	Q1ea13 coccidioides

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OM protein - protein search, using sw model

Run on: November 15, 2007, 08:50:16 ; Search time 265 Seconds
(without alignments)
88.954 Million cell updates/sec

Title: US-10-568-108-2

Perfect score: 109

Sequence: 1 GAYDLRRRERQSLRRRERQSR 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_8.4:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
--------	-------	-----	-------	-------	--------	----	----	-------------

1	66	60.6	226	2	Q86SR2_HUMAN			Q86sr2 homo sapien
2	66	60.6	251	1	CAP7_HUMAN			P20160 homo sapien
3	61	56.0	1109	2	Q4BRC8_BURVI			Q4brc8 burkholderi
4	58	53.2	785	2	Q3JNU7_BURP1			Q3jnu7 burkholderi

5	57	52.3	386	2	Q29RC7_BRARE	Q29rc7 brachydanio
6	57	52.3	1117	2	Q7RHG1_PLAYO	Q7rhg1 plasmodium
7	55	50.5	336	2	Q1LJA3_RALME	Q1lja3 ralstonia m
8	54	49.5	77	1	PRT2_SEPOF	P80002 sepio offic
9	54	49.5	167	2	Q71RF1_HUMAN	Q71rf1 homo sapien
10	54	49.5	167	2	Q7Z780_HUMAN	Q7z780 homo sapien
11	54	49.5	194	2	Q9W1I6_DROME	Q9w1i6 drosophila
12	54	49.5	227	2	Q4RWW6_TETNG	Q4rww6 tetraodon n
13	54	49.5	237	2	Q98SE2_CHICK	Q98se2 gallus gall
14	54	49.5	238	1	U2AF1_MOUSE	Q9d883 mus musculu
15	54	49.5	239	1	U2AF1_HUMAN	Q01081 homo sapien
16	54	49.5	239	2	Q3KR55_RAT	Q3kr55 rattus norv
17	54	49.5	240	2	Q701P4_HUMAN	Q701p4 homo sapien
18	54	49.5	245	2	Q32NM8_XENLA	Q32nm8 xenopus lae
19	54	49.5	973	2	Q25VT3_MYCVN	Q25vt3 mycobacteri
20	54	49.5	1450	2	Q2H922_CHAGB	Q2h922 chaetomium
21	54	49.5	1867	2	Q19PP0_POPTR	Q19pp0 populus tri
22	54	49.5	1886	2	Q4SLF6_TETNG	Q4slf6 tetraodon n
23	53.5	49.1	176	2	Q5QMK8_ORYSA	Q5qmk8 oryza sativ
24	53	48.6	60	1	HSP1_MACAG	P42137 macropus ag
25	53	48.6	61	1	HSP1_MACEU	P42138 macropus eu
26	53	48.6	175	1	IF3_AQUAE	O67653 aquifex aeo
27	53	48.6	185	2	Q293G4_DROPS	Q293g4 drosophila
28	53	48.6	227	2	Q4SMD2_TETNG	Q4smd2 tetraodon n
29	53	48.6	249	2	Q8JHJ3_BRARE	Q8jhj3 brachydanio
30	53	48.6	250	2	Q4G0A1_BRARE	Q4g0a1 brachydanio
31	53	48.6	394	2	Q3JHD3_BURP1	Q3jhd3 burkholderi
32	53	48.6	550	2	Q2QXR6_ORYSA	Q2qxr6 oryza sativ
33	53	48.6	640	2	Q2S5C1_SALRD	Q2s5c1 salinibacte
34	53	48.6	957	1	PG03_MYCTU	P56877 mycobacteri
35	53	48.6	2002	2	Q2S5B6_SALRD	Q2s5b6 salinibacte
36	52.5	48.2	526	2	Q2KG03_MAGGR	Q2kg03 magnaporthe
37	52	47.7	63	1	HSP1_HYPMS	Q9glq1 hypsiprymno
38	52	47.7	118	2	Q7M4A3_LOLPE	Q7m4a3 loligo peal
39	52	47.7	175	2	Q5YPL2_NOFCFA	Q5ypl2 nocardia fa
40	52	47.7	285	2	Q90626_CHICK	Q90626 gallus gall
41	52	47.7	286	2	Q84Q43_ORYSA	Q84q43 oryza sativ
42	52	47.7	292	1	SEN34_ASHGO	Q754t3 ashbya goss
43	52	47.7	298	2	Q292D3_DROPS	Q292d3 drosophila
44	52	47.7	311	2	Q6C9Y5_YARLI	Q6c9y5 yarrowia li
45	52	47.7	372	2	Q6DUB6_PIG	Q6dub6 sus scrofa
46	52	47.7	420	2	Q92JW9_RHIME	Q92jw9 rhizobium m
47	52	47.7	523	2	Q5RHP5_BRARE	Q5rhp5 brachydanio
48	52	47.7	527	1	GCP60_HUMAN	Q9h3p7 h golgi res
49	52	47.7	654	2	Q6ZRQ7_HUMAN	Q6zrq7 homo sapien
50	52	47.7	724	2	Q868S9_ANOGA	Q868s9 anopheles g

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OM protein - protein search, using sw model

Run on: November 15, 2007, 08:50:07 ; Search time 172 Seconds
(without alignments)
45.575 Million cell updates/sec

Title: US-10-568-108-1

Perfect score: 76

Sequence: 1 LRRERQSRRLRERQSR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	

1	76	100.0	16	9	ADY21198	Ady21198 Human cel
2	76	100.0	16	9	ADY21240	Ady21240 Gram-nega
3	76	100.0	16	9	ADY29687	Ady29687 Antibacte
4	76	100.0	17	9	ADY21208	Ady21208 Human cel
5	65.5	86.2	17	4	AAG67730	Aag67730 Peptide H
6	65.5	86.2	17	6	ABP59497	Abp59497 Human hep
7	61.5	80.9	22	9	ADY21199	Ady21199 Human cel
8	61.5	80.9	22	9	ADY21241	Ady21241 Gram-nega
9	61.5	80.9	22	9	ADY29688	Ady29688 Antibacte
10	61.5	80.9	23	9	ADY21209	Ady21209 Human cel
11	52	68.4	476	4	ABB65935	Abb65935 Drosophil
12	51	67.1	541	2	AAW37148	Aaw37148 Mammalian
13	51	67.1	783	2	AAW37151	Aaw37151 Mouse neu
14	51	67.1	787	2	AAW37152	Aaw37152 Mouse neu
15	51	67.1	801	8	ADQ97686	Adq97686 Mouse can
16	51	67.1	802	2	AAW37153	Aaw37153 Mouse neu
17	51	67.1	802	4	AAU09139	Aau09139 Mammalian
18	50	65.8	390	3	AAB58287	Aab58287 Lung canc
19	50	65.8	467	7	ADM04921	Adm04921 Human pro
20	50	65.8	467	9	AEC87851	Aec87851 Human cDN
21	50	65.8	472	3	AAB23039	Aab23039 Human AVE
22	50	65.8	472	6	ADA23299	Ada23299 Human SEC
23	50	65.8	491	3	AAB23040	Aab23040 Human AVE
24	50	65.8	491	6	ADA23301	Ada23301 Human SEC
25	50	65.8	537	8	ADQ97689	Adq97689 Human can
26	50	65.8	570	9	AED84702	Aed84702 Ponsin in
27	50	65.8	719	8	ADQ97691	Adq97691 Human can
28	49	64.5	1898	2	AAV30795	Aay30795 A human t
29	49	64.5	1898	7	ADD48869	Add48869 Human Pro
30	49	64.5	1898	10	AEK65354	Aek65354 Human tri
31	48	63.2	70	9	AEC62684	Aec62684 PAP7 upst
32	48	63.2	97	3	AAB43257	Aab43257 Human ORF
33	48	63.2	126	8	ADY22957	Ady22957 Plant ful
34	48	63.2	319	6	ABU70389	Abu70389 Human adi
35	48	63.2	364	8	ADS34465	Ads34465 POSH prot
36	48	63.2	364	8	ADU69062	Adu69062 Human GOC
37	48	63.2	528	4	AAM78918	Aam78918 Human pro
38	48	63.2	528	8	ADS34467	Ads34467 POSH prot
39	48	63.2	528	8	ADS34466	Ads34466 POSH prot
40	48	63.2	528	8	ADS34464	Ads34464 POSH prot
41	48	63.2	528	8	ADU69063	Adu69063 Human GOC

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OM protein - protein search, using sw model

Run on: November 15, 2007, 08:50:07 ; Search time 236 Seconds
(without alignments)
45.575 Million cell updates/sec

Title: US-10-568-108-2

Perfect score: 109

Sequence: 1 GAYDLRRRERQSRRLRRERQSR 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID

						Description
No.	Score	Match	Length	DB	ID	
1	109	100.0	22	9	ADY21199	Ady21199 Human cel
2	109	100.0	22	9	ADY21241	Ady21241 Gram-nega
3	109	100.0	22	9	ADY29688	Ady29688 Antibacte
4	109	100.0	23	9	ADY21209	Ady21209 Human cel
5	66	60.6	22	9	ADY21246	Ady21246 Gram-nega
6	66	60.6	22	9	ADY29693	Ady29693 Antibacte
7	66	60.6	197	1	AAP91931	Aap91931 Human hep
8	66	60.6	199	7	ADF17970	Adf17970 Human cat
9	66	60.6	199	7	ADG42089	Adg42089 Human cor
10	66	60.6	200	8	ABM84641	Abm84641 Human dia
11	66	60.6	221	2	AAR84663	Aar84663 Human hep
12	66	60.6	221	2	AAW04875	Aaw04875 Heparin b
13	66	60.6	222	2	AAR41935	Aar41935 Recombina
14	66	60.6	222	2	AAW73210	Aaw73210 CAP37 pro
15	66	60.6	222	7	ADG42088	Adg42088 Human pol
16	66	60.6	225	2	AAW88362	Aaw88362 Human mat
17	66	60.6	225	2	AAY21551	Aay21551 Human hep
18	66	60.6	225	2	AAW88118	Aaw88118 Mature hu
19	66	60.6	225	3	AAY71881	Aay71881 Human hep
20	66	60.6	225	3	AAY71882	Aay71882 Human hep
21	66	60.6	225	3	AAY71883	Aay71883 Human hep
22	66	60.6	225	3	AAY71876	Aay71876 Human mat
23	66	60.6	225	4	AAY71891	Aay71891 Human mat
24	66	60.6	225	7	ADE11587	Ade11587 Human mat
25	66	60.6	225	7	ADE11551	Ade11551 Human mat
26	66	60.6	225	8	ADK42019	Adk42019 Human hep
27	66	60.6	225	9	ADV21099	Adv21099 Human azu
28	66	60.6	225	9	ADX69310	Adx69310 Human hep
29	66	60.6	225	9	ADY82139	Ady82139 Human hep
30	66	60.6	225	10	AEJ02080	Aej02080 Human mat
31	66	60.6	226	2	AAR10669	Aar10669 Cationic
32	66	60.6	228	7	ADE11545	Ade11545 Human mat
33	66	60.6	232	2	AAW88364	Aaw88364 Human pro
34	66	60.6	232	2	AAY21550	Aay21550 Human hep
35	66	60.6	232	2	AAW88120	Aaw88120 Human hep
36	66	60.6	232	3	AAY71877	Aay71877 Human pre
37	66	60.6	232	10	AEJ02083	Aej02083 Human mat
38	66	60.6	238	7	ADE11549	Ade11549 Human mat
39	66	60.6	244	4	AAY71893	Aay71893 Human pre
40	66	60.6	245	7	ADE11547	Ade11547 Human mat
41	66	60.6	251	2	AAR10668	Aar10668 Cationic

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OM protein - protein search, using sw model

Run on: November 15, 2007, 08:50:15 ; Search time 13 Seconds
(without alignments)
121.875 Million cell updates/sec

Title: US-10-568-108-1

Perfect score: 76

Sequence: 1 LRRERQSRRLRERQSR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	49	64.5	1898	1	A45973			trichohyalin - hum
2	48	63.2	1094	2	A53435			vesicular transpor

3	46	60.5	675	2	D83405	conserved hypothet
4	46	60.5	699	2	E84565	hypothetical prote
5	45	59.2	1027	2	T46481	hypothetical prote
6	45	59.2	1233	2	T30989	serine/threonine p
7	45	59.2	3498	2	T22330	hypothetical prote
8	44	57.9	36	2	JA0173	basic peptide - wi
9	44	57.9	263	2	B84778	hypothetical prote
10	44	57.9	454	2	T19433	hypothetical prote
11	44	57.9	679	2	T00636	hypothetical prote
12	44	57.9	1407	1	S28589	trichohyalin - rab
13	43	56.6	118	2	S56117	spermatid-specific
14	43	56.6	308	2	F95416	hypothetical prote
15	43	56.6	413	2	H88481	protein let-756 [i
16	43	56.6	427	2	AE2512	hypothetical prote
17	43	56.6	444	2	T32648	hypothetical prote
18	43	56.6	468	1	FOMVMU	gag polyprotein -
19	43	56.6	538	1	FOMVM	gag polyprotein -
20	43	56.6	569	2	T43531	probable potassium
21	43	56.6	733	2	G84668	hypothetical prote
22	43	56.6	1175	2	T22491	hypothetical prote
23	42	55.3	58	2	S34045	protamine - North
24	42	55.3	78	2	A40973	spermatid-specific
25	42	55.3	79	2	S56116	spermatid-specific
26	42	55.3	99	2	B46598	ski-related protei
27	42	55.3	126	2	S58321	probable membrane
28	42	55.3	296	2	S73007	hypothetical prote
29	42	55.3	513	2	T03916	hypothetical prote
30	42	55.3	614	2	AB2304	two-component hybr
31	42	55.3	684	1	TVHUSN	transforming prote
32	42	55.3	690	2	I51298	transforming prote
33	42	55.3	704	2	T24517	hypothetical prote
34	42	55.3	710	2	AE1956	hypothetical prote
35	42	55.3	737	2	T15597	hypothetical prote
36	42	55.3	749	2	T08101	outer dynein arm d
37	42	55.3	788	2	G89901	hypothetical prote
38	42	55.3	810	2	T44430	protein PV100 [imp
39	42	55.3	919	2	F81998	ribonuclease E (EC
40	42	55.3	919	2	F81225	ribonuclease E NMB
41	42	55.3	1017	2	T15598	hypothetical prote
42	42	55.3	1131	2	S22266	FUN30 protein - ye
43	42	55.3	2550	2	B53435	vesicular transpor
44	41	53.9	45	2	B58208	protamine II-1 - p
45	41	53.9	47	2	F58208	protamine II-5 - p
46	41	53.9	47	2	E58208	protamine II-4 - p
47	41	53.9	142	2	B72667	hypothetical prote
48	41	53.9	227	2	T46264	hypothetical prote

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: November 15, 2007, 08:50:15 ; Search time 17 Seconds
(without alignments)
121.875 Million cell updates/sec

Title: US-10-568-108-2

Perfect score: 109

Sequence: 1 GAYDLRRRERQSRRLRRERQSR 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB ID	
1	66	60.6	251	1 TRHUAZ	azurocidin precurs
2	54	49.5	77	2 B40973	spermatid-specific

3	54	49.5	240	2	A46179	U2 snRNP auxiliary translation initia
4	53	48.6	175	2	C70453	hypothetical glyci
5	53	48.6	957	2	D70835	spermatid-specific
6	52	47.7	118	2	S56117	ribonucleoprotein
7	52	47.7	285	2	S53710	PE38 orf153 - Bomb
8	51	46.8	309	2	T41889	hypothetical prote
9	51	46.8	2019	2	T27702	protamine III - Am
10	49	45.0	43	2	D58213	conserved hypothet
11	49	45.0	261	2	AB3070	hypothetical prote
12	49	45.0	319	2	H98216	trichohyalin - rab
13	49	45.0	1407	1	S28589	basic peptide - wi
14	48	44.0	36	2	JA0173	arginine-rich prot
15	48	44.0	234	2	S27956	hypothetical prote
16	48	44.0	294	2	E87538	protein-lysine 6-o
17	48	44.0	420	2	A45166	l-caldesmon, nonmu
18	48	44.0	517	1	A39038	trophoblast-endoth
19	48	44.0	550	2	A46419	gene XE7 protein -
20	48	44.0	695	2	I54325	h-caldesmon - chic
21	48	44.0	771	1	A33430	SWH1 protein homol
22	47.5	43.6	694	2	T07638	protamine B - Russ
23	47	43.1	27	1	SRAPC	protamine St2b - h
24	47	43.1	58	2	S10755	protamine St2a - h
25	47	43.1	62	2	S10754	spermatid-specific
26	47	43.1	78	2	A40973	spermatid-specific
27	47	43.1	79	2	S56116	protamine - boll w
28	47	43.1	132	2	S10305	U1 snRNP 70K prote
29	47	43.1	378	2	S04336	hypothetical prote
30	47	43.1	406	2	T24492	caldesmon, non-mus
31	47	43.1	531	2	A55887	hepatoma-derived g
32	47	43.1	669	2	JC5662	serine/threonine p
33	47	43.1	728	2	T43632	serine/threonine p
34	47	43.1	792	2	T43630	caldesmon - human
35	47	43.1	793	1	JH0628	hypothetical prote
36	47	43.1	1075	2	T27623	hypothetical prote
37	47	43.1	1080	2	T27622	trichohyalin - she
38	47	43.1	1549	1	A40691	protamine II - Ame
39	46.5	42.7	56	2	C58213	probable membrane
40	46	42.2	126	2	S58321	conserved hypothet
41	46	42.2	224	2	F69444	immediate-early pr
42	46	42.2	321	1	A43681	hypothetical prote
43	46	42.2	321	2	C72869	hypothetical prote
44	46	42.2	354	2	T27099	aspartate-tRNA lig
45	46	42.2	580	1	S33743	hypothetical prote
46	46	42.2	651	2	T15624	protein kinase (EC
47	46	42.2	768	2	H54024	protein kinase - c
48	46	42.2	772	2	I50463	